

In the Claims:

Please cancel claims 1-22, 24, 26-28, and 30-36. Please amend claims 23, 25, and 29 as indicated below. Please add new claims 37-59. A list of claims and their status is shown herein.

1-22 (Canceled)

23. (Currently Amended) A method for altering fatty acid composition in plant seeds, comprising the steps of:

a) introducing a recombinant nucleic acid construct into a plant, said construct comprising at least one seed-specific regulatory sequence operably linked in sense orientation to a ~~mutant~~ full length delta-12 fatty acid desaturase mutant gene, wherein said mutation is in a (Ala/Gly)His(Asp/Glu)CysGlyHis conserved sequence; and

b) obtaining progeny from said plant, said progeny producing said seeds having an oleic acid content of from about 69% to about 90% ~~-said altered fatty acid composition; and~~

e) ~~producing seeds having said altered fatty acid composition.~~

24. (Canceled)

25. (Currently Amended) The method of Claim 23, wherein said ~~altered fatty acid composition comprises~~ progeny produce seeds having a decreased level of linoleic acid content of from about 1.0% to about 10.0%.

26-28. (Canceled)

29. (Currently Amended) A recombinant nucleic acid construct effective for decreasing linoleic acid content when expressed in seeds, said construct comprising at least one seed-specific regulatory sequence operably linked in sense orientation to a mutant delta-12 fatty acid desaturase encoding a delta-12 fatty acid desaturase gene equivalent product having at least one mutation which renders said desaturase gene product non-functional, said mutation being in a His-X-Cys-Y-His (SEQ ID NO:17) amino acid region, wherein X is selected from the group consisting of Asp and Glu and Y is selected from the group consisting of Gly and Ala.

30-36. (Canceled)

37. (New) The method of Claim 23, wherein said mutation in said delta-12 fatty acid desaturase mutant gene is in a Ala-His-Glu-Cys-Gly-His conserved sequence.

38. (New) The method of Claim 37, wherein said conserved sequence in said delta-12 fatty acid desaturase mutant gene is Ala-His-Lys-Cys-Gly-His.

39. (New) The method of Claim 23, wherein said seeds have an oleic acid content of from about 74% to about 90%.

40. (New) The method of Claim 39, wherein said seeds have an oleic acid content of from about 80% to about 90%.

41. (New) The method of Claim 39, wherein said seeds have an oleic acid content of from about 75% to about 88%.

42. (New) The method of Claim 41, wherein said seeds have an oleic acid content of from about 80% to about 88%.

43. (New) The method of Claim 23, wherein said seeds have an α -linolenic acid content of from about 1.0% to about 10.0%.

44. (New) The method of Claim 25, wherein said seeds have a linoleic acid content of from about 1% to about 6%.

45. (New) The method of Claim 23, further comprising the step of introducing a recombinant nucleic acid construct into said plant, said construct comprising at least one seed-specific regulatory sequence operably linked in sense orientation to a delta-15 fatty acid desaturase mutant gene having a mutation in a (Ala/Gly)His(Asp/Glu)CysGlyHis conserved sequence.

46. (New) The method of Claim 45, wherein said mutation in said delta-15 fatty acid desaturase mutant gene is in a Gly-His-Asp-Cys-Gly-His conserved sequence.

47. (New) The method of Claim 46, wherein said conserved sequence in said delta-15 fatty acid desaturase mutant gene is Gly-His-Lys-Cys-Gly-His.

48. (New) The method of Claim 45, wherein said seeds have an α -linolenic acid content of from about 1% to about 5%.

49. (New) The method of claim 23, wherein said plant is soybean.

50. (New) The method of claim 23, wherein said plant is rapeseed.
51. (New) The method of claim 23, wherein said plant is cotton.
52. (New) The method of claim 23, wherein said plant is corn.
53. (New) The method of claim 23, wherein said plant is safflower.
54. (New) The method of claim 23, wherein said seed-specific regulatory sequence is a bean β -phaseolin promoter.
55. (New) The method of claim 23, wherein said seed-specific regulatory sequence is an α subunit of soybean β -conglycinin promoter.
56. (New) The method of claim 23, wherein said seed-specific regulatory sequence is maize 18 kd oleosin promoter.
57. (New) The method of claim 23, wherein said seed-specific regulatory sequence is maize 15 kd zein promoter.
58. (New) The method of claim 23, wherein said seed-specific regulatory sequence is a *Brassica napin* promoter.
59. (New) A method of making a vegetable oil, comprising extracting said oil from seeds of one or more plants, said plants having a recombinant nucleic acid construct comprising at least one seed-specific regulatory sequence operably linked in sense orientation to a delta-12 fatty acid desaturase gene having a mutation in a (Ala/Gly)His(Asp/Gln)CysGlyHis conserved sequence, where said oil has a linoleic acid content of from about 1.0% to about 10.0%.